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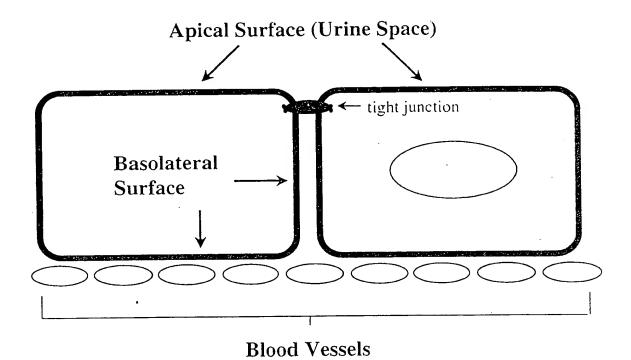


FIG.1

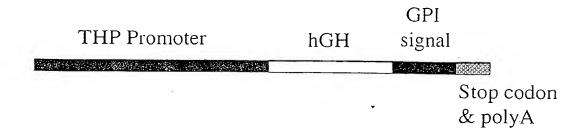


FIG.2

	1				★ 50
Rat		TWLLLVMVVT	PWFTVAGAND	SPEARRCSEC	HUNATCVLDG
Mouse	MGIPL	TWMLLVMMVT		STEARRCSEC	HINATCTVDG
Human	MGQP.SL	TWMLMV.VVA	(SWFITTAATD	TSEARWCSEC	HSNATCTEDE
Bovine	MKCLFSP.NF	MWM.AA.VVT	SWVIIPAATD		HSNATCTVDG
	51			*	100
Rat	VVTTCSCQAG	FTGDGLVCED	IDECATPWTH		TLGSYECSCQ
Mouse	VVTTCSCQTG	FTGDGLVCED FTGDGLTCVD	MDECATPWTH LDECAIPGAH	NCS NSSCVN	TPGSFKCSCQ TPGSFSCVCP
Human Bovine	AVTTCTCQEG AATTCACQEG	FTGDGLECVD		NCSATKSCVN	
Bovine	101	1 IGDGBECVD	DDECAVEGAL	Medaliksevi	150
Rat		CIDVNECTEO	GLSNCHSLAT	CVNTEGSYSC	VCPKGYRGDG
Mouse	DGFRLTPGLG	CTDVDECSEQ	GLSNCHALAT	CVNTEGDYLC	VCPKGFTGDG
Human	EGFRLSPGLG	CTDVDECAEP	GLSHCHALAT	CVNVVGSYLC	VCPAGYRGDG
Bovine	EGFLLSSELG	CEDVDECAEP	GLSRCHALAT	CINGEGNYSC	VCPAGYLGDG
<b>.</b> .	151	= nor nor noa	DCGWI WGODD	CAR EXEMI MEN	200
Rat	WYCECSPGFC	EPGLDCLPQG EPGLDCLPQG	PSGKLVCQDP PDGKLVCQDP		WRSTDYGAGY WRSTEYGVGY
Mouse	WYCECSPSSC WHCECSPGSC	GPGLDCVPEG	DALVCADP		WRSTEYGEGY
Human Bovine	RHCECSPGSC	GPGLDCVREG	. DALVCVDP		WRSTEYGSGY
2011.0	201	0.0		*	
Rat	SCDSDMHGWY	RFTGQGGVRM	AETCVPVLRC	NTAAPMWLNG	SHPSSREGIV
Mouse	SCDAGQHGWY	RFTGQGGVRM	AETCVPVLAC		SHPSSSEGIV
Human	ACDTDLRGWY	RFVGQGGARM		NTAAPMWING	THPSSDEGIV
Bovine	ICDVSLGGWY	RFVGQAGVRL	PETCVPVLHC	NTAAPMWING	THPSSDEGIV
	`251	**************	THE OPCORUM	**	300 LAYCTDPSSV
Rat	SRTACAHWSD SRTACAHWSD	HCCLWSTEIQ	VKACPGGFYV	£ 6	LAYCTDPSSV
Mouse Human	SRKACAHWSG		VKACAGGYYV	YNLTAPPECH	
Bovine	NRVACAHWSG			YNLTAPPECH	
20120	301		<b>,</b>		350
Rat	EGTCEECGVD	EDCVSDNGRW	RCQCKQDFNV	TOVSLLEHRL	ECEANEIKIS
Mouse	EGTCEECRVD	EDCISDNGRW		TOVSQLEYRL	ECGANDIKMS
Human	EGTCEECSID	EDCKSNNGRW	HCOCKODENI	TDISLLEHRL	ECGANDMKVS
Bovine	EGTCEECRVD	EDCKSDNGEW	HCQCKQDF <u>NV</u>	<u>T</u> DLSLLERRL	ECGVDDIKLS
D - 6	351	ENGINEMANT NID	ROCSGFSERG	ERDWMSIVTP	400 ARDGPCGTVL
Rat Mouse	LSKCQLQSLG LRKCQLQSLG	FMKVFMYLND FMNVFMYLND	ROCSGFSESD	ERDWMSIVTP	ARNGPCGTVL
Human	LGKCQLKSLG	FDKVFMYLSD	SRCSGFNDRD	NRDWVSVVTP	ARDGPCGTVL
Bovine	LSKCOLKSLG	FEKVFMYLHD	SQCSGFTERG	DRDWMSVVTP	ARDGPCGTVM
	401 <del>X</del>			•	450
Rat	RENETHATYS	NTLYLASEII	IRDINIRINF	ECSYPLDMKV	SLKTSLQPMV
Mouse	RENETHATYS	NTLYLANAII	IRDIIIRMNF	ECSYPLDMKV	SLKTSLQPMV
Human	TRNETHATYS	NTLYLADEII	IRDLNIKINF	ACSYPLDMKV	SLKTALQPMV
Bovine	TRNETHATYS	NTLYLADEII	IRDLNIRINF	ACSYPLDMKV	SLKTSLQPMV 500
Rat	451 SALNIELGGT	GKFTVOMALF	ONPTYTOPYO	GPSVMLSTEA	
Mouse	SALNISLGGT	GKFTVRMALF	QSPTYTQPYQ	GPSVMLSTEA	
Human	SALNIRVGGT			GSSVTLSTEA	
Bovine	SALNISMGGT	GTFTVRMALF		GSSVTLSTEA	
	501	_ :	<u>*</u> _		550
Rat	GDLSRFVLLM				
Mouse	GDLSRFVLLM				
Human	GDLSRFALLM				
Bovine	GDLSRFVLLM	TNCYATPSSN	ATOPLKYFII	QDRCPRAADS	
Dat	551	RFAGNSDLVY	LUCETALCOT	MSEOCKDECS	600
Rat Mouse		RFAGNYDLVY			
Human		RFAGNYDLVY			
Bovine		RFAGNYDLVY			
	601	_	_		648
Rat	DQTRVLNLGP				
Mouse	DQTRVLNLGP				
Human	DQSRVLNLGP		<del></del>		-
Bovine	DQTRVLNLGP	ITRKGGQAAM	<u>SRA</u> APSSLGL	LQVWLPLLLS	ATLTLMSP

FIG.3

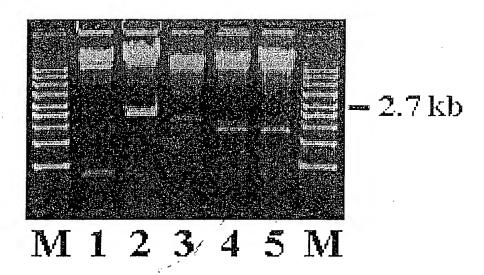
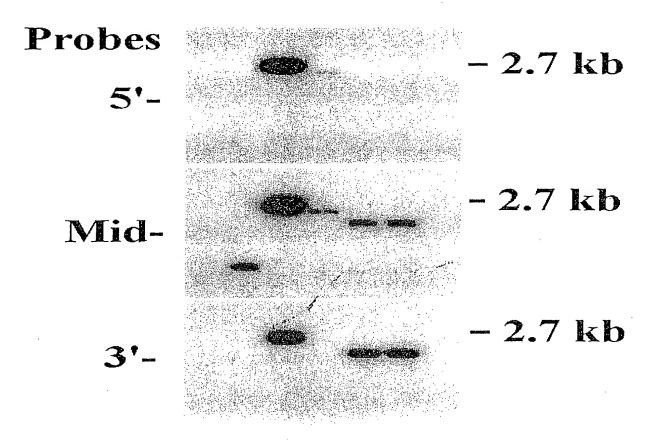


FIG.4



M 1 2 3 4 5 M

FIG.5

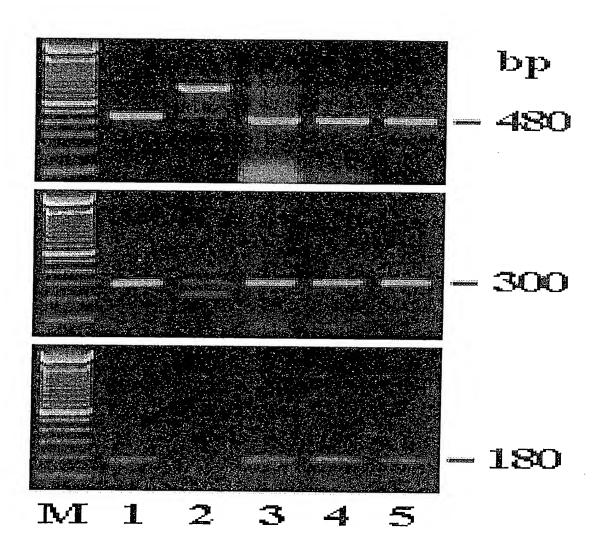


FIG.6

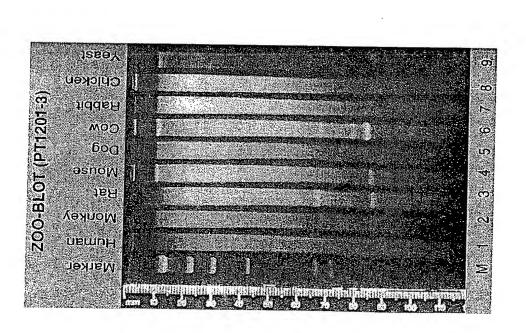
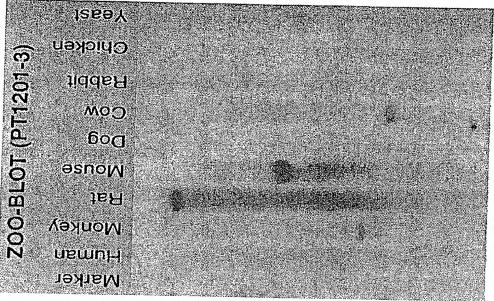


FIG. 7A



M 1 2 3 4 5 6 7 8

FIG. 7B

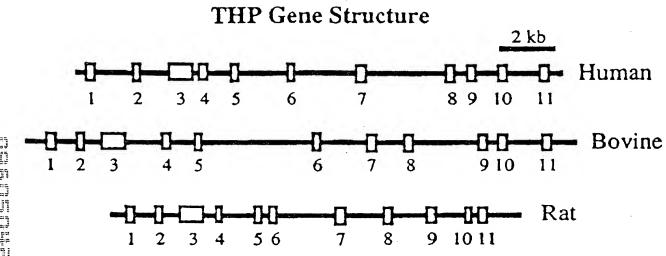


FIG.8

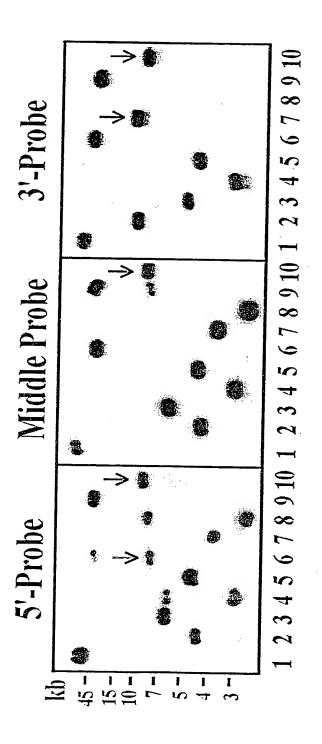


FIG.

GGGG/GGCCC TCGGGAGTTT GGCTAAGTCT TGCAAATGAG CTGTGATGAC polycloning site of pBS AGGTTTGCGC CATATGAGAT CCAGTGACAA GCTCATCTCT AGATGTCTGC 51 ATACCAATAA GTGACCCATC ATTATGCAAT CAGGCCGGAC TCATCCTCTG 101 151 TGGCTTTGTC TCTTACTACT GTAAACTTGA TAACCTATAT GATTTTACCC ATTTCCCCTC CATGGCACTC AACTCTCCTC TTCCTATGTG ACCCTACTTA 201 TGTCCTATGT GACTCCAGCT GCTTCCTTTG ATGAGAGCCA TCCTGTTCTT 251 JP.S3 301 TCTATGTGAC TCTGCTCACT TCTTCCACGT GACTCCACCA ATCTGTCTAC ATTGCAGAGT CACTCACAGT TTCTTGAGAG CAGAAGACTC AGAACTGATC 351 TGTCCTCAAT GTCCTCCCTA CACTTTCTCC TCATAATCCA CATATCTAAA 401 451 GCTATAGAGA TAATTTCATG CACTATAGCT TTCAGTACTA TCGTATCTAC 501 TGTCTCTACC CTGTAACTGG TATCTTCATG ACATCTCGAA TATTTCCAAT 551 TTCTCTATTG CTGCAAAGTC TTGAGAAGTC TAGTCTTATG GATCTCCTTT TCTCCTCAGG TCTCCTGGTC TCCACACAC ATTCACACTT CTTGAATATT 601 JP.S4 CTTTGAACAT AACAAATTCT CTCCATGGGT TTGTTCCCTC TACCCAAATT 651 CATGCCTTCA GGATACTTAC TCTGCCCCAT CTTCACTCAT CTCTGCTTTG 701 751 GTCATTCAAA TCTCAAATGT AGCCATTTCT AAAAGGCTCT CCAAGAGAAT AATATTTGAA AGCATTTTGC TATTCTATCA AGTGATCATA CAATGTCTGC 801 TCCTGCCACC ACCATGACCA TCCCCATGAA TACAGACACT GCCTTCTTAG 851 JP.S5 TGTTTGCTGT ATGTGTTCTG TGTGGTACAT TGTAGATAAA TGCTGTAATA 901 AACATCTGTG GAGCAAATTG AATCATCAGA TAGCACCCTC TCTCTGAGAG 951 GCATGATCTC ATGGTTATCC CCAAAGCATG AGGTAAGGAC ATTATCCCAG 1001 GTCCATGCTG GTTTCCGTAT TGATTGTTTC TAACACAAAC TTAATAGATT 1051 AAAACAGCAC GGATTTATTC TCACATGTTT TGAGACGCCA GAAATCTGAC 1101

. . .

FIG. 10A

ACCAGTTTCA ATGTTTAGAC TTGATGCACA CCTGTAATTC TGGTACTTAG 1151 GAGGCAGATG CAGGGGGACT ATGATTTAAA GCCCATTTTT AAGCTGCTGG 1201 GTGAGAACCT GTCTTGATTT TTTTTTCACA TTGGGCTAAA AGTCAAGGAT 1251 CATCAGGGTT GGTGCATTCT GGAAGAAACC TTTGCCTTGC AGCTTCCCAG 1301 1351 AGGGCCGCCA GCATTCCTTG GCTTGTGTTT GGTCCTGGAA TCACTGTGAC CTTATGCTCC ATCCTCACAT TCCCTCTGCA TTTATCCTCT AAGCACCGGT 1401 JP.S6 1451 GTGCTTGTAT CCAACCTTTA GGAGCCCCAT AGATCCCCCA TTTCTCCTCG 1501 ACTTAATCAC ACCTGTATAA GTACTTTTCA CTCTGCAAAG CAATATTTGT GGGTCCAAGG GATTAGGATG TGGGTATATT TGTGGGGTGT CATTATTCAA 1551 TGCTTCATAT TTACACTGTT TCTCTGTTTC ACTTTATTGG GGTACTTGAA 1601 1651 CTTCTAAGAA GAACTGAGGG GTATTGTTGT AGGAACTAAA TTCCCCCATG 1701 GACCTCTGTG CTTTCCACCT ATCACACAAG ACAGAGGGTA TTTGTATTTT TAGATCCCCA GAAGAAATTC CCACTCTCAA CCCTCCATCC CTGACTTGCT 1751 CACATCTAGA TGAAGCAGGG AACAGCCTGA GNCCTGGAAC TCACTGGAGC 1801 1851 CAGATGACTC TATGGAGTTA GGTTTTAGTA TTCAAGACAC GATGCAAGAC TCACCTGCCT TCCCCTCACA GACATGTGGC TGCCTGTCAA AGGTGGGGCC 1901 ATGGGGCTGC TGAGACTAAG TCACGTGGAC AGCGCCCATG ACAAGCAGTG 1951 JP.S7 2001 ACATGGAGAC CAAGGCTGCA GTGTGCATGC TCCACAGGTG CACCTGAAGC 2051 CTCAGAGACG GGAAGAGGAG AGGGAGCAGA AAGATGGGGT ACAGATACCC 2101 CTCTGTTAGG AAGGGCTTCA AAACCGTCTT CTAAGTTTTT GATCCTTTTA 2151 AATGTATCCA CCTGTCACTT GACCCTCTCC TGCTCTGTCT GATCAGCTTC 2201 TCAAAACCCT TCATCCCCTT AACTCCACCC TACTGAAAAA AGATGAAACC 2251 ACTTGTCAAT ATAAACCTCA ACAGCTAAGC ATGGAATACT GTTAACCCCT CAAGACATAA AGCTGACTGA AGGGATAAGT TTGAAAAAAA TGGGCTTCAG 2301 2351 TTTGCACTAG CTAAGTATGT AACCTTGAAG ATATTACTCA GTTTCTCTGA ACTTCAGTCT GCTCTCCTAT TTATTGACAA CATGTAAGAG CACATACCGG 2401 GCATTTCTTG TCACCAAATG AAGTTTCCAG TACCAGGAAT GGGTTATATC 2451

FIG. 10B

TAATCGAGTT GTTGGCCAAA GGAGTTCCAT GGAAACTCCC AAACAATCCA 2501 GGCTATTGGC AAGACTTTTG ATGTCTCTCC ACAAACTGAC AGCAACTGTT 2551 GAAAGACAAT ACCTACACAG CTCACTGAAC ACAGAGAAGC TGAGTTGGTG 2601 2651 CCTACATAAA TCCTCTAGCT CTATGAAGGT CCATAATGGT ATTCATGGCC 2701 CTAGAAGATA CTCTTCCCTC CACCAAAGGA GAAATGTAAA CACTAAGCCA 2751 GCCATAAACC CTTTGGTCTG TTAGAGTGGC CTGCCTGCAA GTTCTGCTGG TGTAATAATG GCACAGAGCT TGTAGGAGTA ACCAAACAAT ATCTGATAGG 2801 TTAAGGCCCA CTCCATGAGA TCAAACCCAG ACCTAACAAC ACTTGGGTGG 2851 2901 ATGAGAACCC GAGACCAGAT AGGCCAGGGA CCTATGGGAA AACTAAACAT GACTGTTCTG CTAAAAGAAC CTACCAATAA AATAGCTCCT AGTGACATTC 2951 3001 TGCCATATTT <u>ATAGATCAGT TCCTTGTTCA</u> TCCATCATCA GAAAACTTCC JP.AS14 TCTTCAGTAG ATAGAAACAA ATATAGAGCC CACAGCCAGA TAATATCCAG 3051 AGAGTGAGAT ACCCTGGAAC ACTCAGCTCT AAAAGGGATG TCTCCATCAA 3101 3151 CCCCCCCC CCCACCTTT CAGGACTCAT GAAACCCTCC AGAAGACGAG 3201 TCAGAAAGAG TGTAAGATCC AGAAGGGATG GAGGACATCC AAAACTTAAG GCCTTCAAGA CACAACTGTA AGGGAACACA TATGAACTTA GAGAGATGGT 3251 3301 GCAGCATGCA CAGAGCCTGC ATGGGCTTGT ACCAGATGGG GTTCTAGAGC 3351 TGAAAGGAGA AATGGATAGC CACTCTGATT CCTAACCCAG AAGTGACCCC 3401 TAACTGATAG TGACTTGCAA ATAAAAAATT AGTCTTTTTT CAAAGGGAGT 3451 CTCACTGGGA AAATAAACCA CTCTAAATAG TAGACCCCAT GCCCAGCAGT 3501 AGATGGCCAA CAGAAAATGA ACTCAATGTC ATCTTTGACC TTCCTTTGTC 3551 GGAAAGCTTT TTGTTTGCTT TTTCTTACCC TACAGGTCCT TTGCATATTT JP.AS13 ATTATGGTTT CTTGTTTCAG GTTTTTAATG GAACTCCTGA GTGTGTGAAT 3601 GTGTGTGTCT CTGCATACAT GTGTGTTTCT TAAGCCCGTT CTTTTCTTT 3651 3701 TCTTCTCTT ATTGTTTAAA AAAACAATTG TTCTTTATTT TATTATTATT CCTTATTTA GACAGAAACA TTGTGGATCC AGATGGGAGA AGAGGTTGGA 3751 3801 GGAATTGGGA GGAGTAAAGG GACAGAAACC ATAATCAGGG GGAACCATAA

FIG. 10C

TCAGGGAGAA CCATAATCAG GGGGAGCCAT AATCAGGGGG AGCCATAATC 3851 CAAGGGAACC ATAATCAGAA TATACTGTAT GAAAAAATT CTATTTTCAA 3901 3951 TAAAAAAAGA ATAAAAAAA AACAGTCTGA CTGAAGAATA GCACTTGGTA AGTAACTCTT GTTATAACAA TCCATATCAA ATGCCCTGCC TGTGTTAGCA 4001 AGTTAAGAGA AAAGATTATT CCAAGAGATC CAAGTCTCCT TCAAAACCAA 4051 ZT.S1 GTGTGTACAG AACATTGTCT GAGGAGTAAG ATTGCATTTG GCAACATGCA 4101 TGTCTTTAAT GGTGTGGAGA ATTTCAGTGG AGTTGGCACG TCAGAAAGCA 4151 JP.AS12 4201 CACTGGTGAA AAATGGAGAG AATAGATATA TCCTTTGAGA AATTTGGTCT 4251 CAAAAAGTAG GGTATCAAAT TACTTGGTGT CTGTGAGATC AATTGGTTGT CTCTGTAGGT TAGCTTACAT AGGAGACAGG AATAAGTGAA GGAGAGAGG 4301 GAGGACATTG GAGCACCCAA GGAGAGAGGG ACCTTCCTCC TAAAAGTGAA 4351 4401 TGAGGTGGCC TTCATTCCAA GGAGAAGAGA TTCAGGTCGC CCGGGAAGAT 4451 GAGGGACCAA CATCCACAAG GAATGGCAGG AAGTCATCCT GTGTGCATAA ATGGAGAGAG GGGGTCAAAG ATGGAGCAAA GAAGGATGAG CAAGAAAATG 4501 4551 GTGGATGTGG ATACTCTGAG GATGGCCTGG CTGTGGTGAG CAAAATGTGG GCAAAGTGGC ACTCCATGAA CAAGACAGCT TGCTCTGTTT GCAGATCCTT 4601 4651 AAATAAAGGC ACATGGCATG CCATGGAGGC TAGGGGGAGTG GAGGGGAAAG 4701 GTATATAGAT AGATGCAGAA GTACCAGAGG AGCCAGGAAG GACAGGAGTA 4751 GGAGGGACAG GTTTGCACAA GGCTTTGTCC TCTCCCCACC AGCTCTCTCT JP.AS11 CCCTTCTGTA TATGCACATA CACAGTGAGC TAGTGTGCAT ATGTGTGCAC 4801 4851 ATATGCATGT GATGAACAGA GGCCAGTCTT GGGTGTCAGT CTTCAGGCCC 4901 TATCTACCTT GTTTTTGAGA CAATCTCACT TGAGTGAGTT GAGTGACTCT 4951 CCTAGTATTC TACAGAGGTT TCCTCAGGTG GGGAGGAATG GGTGGGAGAA 5001 GCAAATTTAA GACTGGTTGA TTTCTTGAAT TTCAGTGGGC TTGGGAAATA 5051 GCAGCTATAT ATTCAGTTTC CTCGTTCCTG GCTGGCTTCC TGGGGTGATC 5101 AGAGCAGAGT ATAGTAGCCC TGTGTGGCAG TCACACCAAG CAGACAGAAG ATAGGGCATG GCTCTGGTGT GGCTGGTAGA CATAGGAAAG GATCCTTGTA 5151

FIG. 10D

GCAAGATGTT TGCCATCTCC AGAGACTTAG ACAGCCCAGG AAAGTTTGTC 5201 CTCCCAGGAC CAGCCAGCAC TGAGACTGGA ATGCATCAAA TCCAGAGACC 5251 JP.AS10 AGAAAGCACG GTGCTAGCAC TTAGGAAGAG ACACTAGCCC AAAGTCTCCT 5301 TGCTCCTGCC TAAAGCTTTG CCAATTCTGC AAACCTTGAA AAATTAGCAT 5351 CTTTAAATTC AGAAGGGATA CAAGAAGAGA ACTTACATGG GACCTTGTAA 5401 5451 AAAAGCATAG GGCATCAGTA ACTAAAGTTA CAAAGATAAC AATCAGTGGT GAGTGAACAA AGGACATGGC CATGTTTTTT TTGTTATGAA ACACACGCAC 5501 AGGCACAGGC ACTCACGTGT GCGCACGCGC GCACACACAC ACACGCGCAC 5551 5601 ACACACAC ACGCATGCAC ACATGCACCA CACACAAACT GCAAAAGTGA ATAAAAAGAT ATTTCTCACT TTGGCAAAGT GGATGGAAAG TTGATCAAAA 5651 TGAAAGTTAT ACTCAGAACT ATTTTGTACT AGAGGGAGGT TATAAATTAT 5701 JP.AS9 5751 TGTTATTGTT ATATTCTATT TTACTGTTTG TGGCAGCCTA AGTTGGTCTT 5801 GAACTCACTA TGAAGCTAGC AATGACCTTG AGCTTCTGAT CCTTATATCT ACACTCTCAA GTGCCCAGAT TATAAGTGTG CACCACTATA CTCAGTTTAT 5851 GCTGTGCTAA GGACTAAGCC CAATTATACA AACACACACA CATATATACA 5901 5951 CACATACACA CACACACA CGTATATATA TGTATATATA TATACATACA TACACACACA CACACATA TATGTAAAAT TTGGGAAGAT ATATCAATCT 6001 6051 TCTTTAAAGT ACATGCTACT TTGGTCCAAA ACTTTCACTT TTAGGAAGTT 6101 AAGAAGGAAG AGACAGAATA AGAGATGTCC CAAGAAAGTC AGTGTGGTTG 6151 TCTTAGTTAT GCTTCCTGCT CAGTCAATGT TTCAGATTTT TCTCAGCACA JP.AS8 6201 ATGACATCTA TTCTATCAAG TTTTTGATAA CTCTTTACAT GGGACTGGGT 6251 GTGGCTTGTG GCTCTAGCTA TTTCTATTTG TGACTGCCTA TCAGCAAAGC 6301 ATCCACTTCA GACTTTGACT CAAACATCAC CAAGTATTCC CACTTGCATT GTCTCTGTTA ACCAGCATCA CTGTTCACAG GGCAGGGCAT CACATCTCAC 6351 6401 AAAGGGAAAG GGAAAGGGAA GAGTTAAATT CCCTGGGATA CTAGTCACGG 6451 TGGACTCAGG CAAACAGCCT CTTCAATTGT AAGATGATTC CCTAGTCCAA 6501 GGACCCTCTA CTGTTTGGAC TCCAGTCTTG TCTGACAGAG GTCCAGTTCA

GGAGTGTCCA GATGGTCTGA TAACCTGATG CCATTCTCAG AGACTCTTTC 6551 CTGTCTGGAA TCTAGTGAGG AGGACTTATC TGGTGAAGCT GTCCTTTAGA 6601 ACAGGAGTGT GTTCCAGTCT TCAAAGCAAA CATTCCTTTT ATCCTAACAC 6651 AGTCTGACTT CAGATATACT GTCTTTTTCC TGGCTCCTTG GGCTTAGGTC 6701 6751 TACCTTGTCC TTGCCCAGGT CCAAGAAAG GCCCAGAACC TTGGCACTGT 6801 TTTGCCAGTT AATGTCTAAC TGAGGAATGT CTTGCTGCCA AAAGGTGAAA ACAGAGACCT TGTATTTCCA GGCACAGGTG TGACCCCAAT GTCAATCATT 6851 6901 TTGTGTCTAA CTCCCAGGGG AAAAACTAAC AACAACAGAC TCATGGCTTG ZT.S3 GAAAAGGTGA ATTCTATGCC AAAAGGGAAG GAAAGTTCTA CCCCCACAGA 6951 ZT.S4 7001 AACAATCTCA GAGGGCAGAA GCAGAGAATA ATCTGAGGGA GAGGGCCAGC 7051 CAAGGGCAGG CAAGTATATA TTGATCACAG GCACTTACTT GTGAATGGAC EXON 1 CAGTCCTGTC CTGGGTTCAG GTAAGGCTGT ATGAAACTGT CACCCCCATA 7101 JP.AS15 TCCACTTCTC CTCTATCTAA TCCCATTATA TTTCAGGGAG GTTGTGGTAG 7151 7201 AAGCTTAGCT TCTGGACACT GGGGTCCCAT GCTAACCTTC ATGGCATCCT 7251 GGTATGCTGC TGTAAAACCT AGGGTAATGC TTGCATCCAT CTGGAATTAT 7301 TTCACCTGTT GCAACCACAA TCATTTTGAA AATACTAGTA TGTATTATAG TTATGTATGT ATATAGAGTT AATCATCTCT AAAGCTCCTT ATCTTTTGCC 7351 ATTTCTTTAC ATGAGTTGTA TGAAGATGTA GACGATATTC ATTATTCTCT 7401 7451 TTGGTATCTA GCACCTTGTT TGGCACATAA TACTACTCAA TAAGGGTTTG 7501 TTGAATGAAT AAGTAGGTGA GAGCAAATTG TAAGTTCAGG TAATCACGAA 7551 CTTCCTGTAA AACTCCAAGG CTGCCTCCAG TAAGGTATAA GTCCTGAGTG 7601 AGCCTTTCCC CATCTTGCAA CTTTTTGCTC CAAATGAAAG ACTCAGTTCT 7651 TCAAAATGTG CAGCACATGG AGGTTTGCGA CATAGGGGTG TATTCACAGA GGCTTCGGAA GCCCACCAAA CCTACAGTTA GATCACTGTA CAGTCTTCCT 7701 TTTACATACA AGCTGTGCCT CCTGGTNTAC ATCCATGCTG TTTTCTGATC 7751 7801 CATATAGAGG GTACACAACA AAAGCATTTC TTCTGTCTAT AGGGAAGCAA ATTAGATCAT GCATGTGCCT CACCCACCTC TGTTCTCATG ATTTCAGGCA 7851

FIG. 10F

EXON 2 7901 TCAGAAACAC AAGGGAAATC CAAAGTACCT AACCCATCCT TGCCTTTGGG 7951 CAGGTGTTTC CAGGACAGAG GGCAGAGTGT AAAGGATGGG GATCCCTTTG 8001 ACCTGGATGC TGCTGGTAAT GATGGTAACC TCCTGGTTCA CTCTGGCTGA 8051 8101 TGTGTGTGT TGTGTAGAGA AATGTTCCCT TTGCAGAAGC AATCTTAATC 8151 CCTCTTTTAG CACACTTGAT GTGATCTTTA TTTTAAGCCC ATTTCTCAGA 8201 TTGTAATGAG CACAGGACTC ACTTCGAAGT TTTGTTAAGA TGCAAATTCT 8251 ACTTTAGTAG GTCTAGCAAG GGG/CCCGAGA CTCTGAATTA ATAGCAGCGT APA/KPN JUNCTION 8301 GTGGGTGATG TTTCTGGTGG GACAAGGGGC TAAAACACCT CTGAACCATT 8351 TCTGCACTTC ACGGTAAAGT CACAAGCATG CCCAGATACA TAAGAGATTT GACCCACCTC TCCTGTAAGT GTGAAGTCAT CCCATGGGGG TAGCTTTGCC 8401 8451 TTCCACCCTG GAGTACTCTG GAATTACACT AAGTATAATT GTGAGGTCAT 8501 GGTTAAAAGC ACATGTTCTG TGGTCAGGCC ATGTGCGTGT ACCCTGTTTG 8551 ACAACTGGCT TGCTCGTTCT GAATGTCAAT ATTCTTTTCT GTAAATGAAG 8601 AAAATGAAAA TGGGTTCCAG CGGCAGGGGG TGTGCCCTGG GGAGGATTCG 8651 CTAAACTCTA GACTGAAAAG TCAATGAATA GAGGACTCCA CTCAGGGGAG 8701 CTCGGATGGG TGTGTTTTGA AGGTGCCAAC AACTTAACAA GTCCAGAAAA 8751 GCAAGAAGT ATGGGCAGGG GCACCTGCCA GCTGCAGGGA TTCTGAAGCT JP.AS5 8801 GGGCTCTTCT GTCCGCAGGA CGGTGTTCTG AATGCCACAA CAACGCCACC EXON 3 8851 TGCACGGTGG ATGGTGTGGT CACAACGTGC TCCTGCCAGA CCGGCTTCAC 8901 TGGTGATGGG CTGGTGTGT AGGACATGGA TGAGTGTGCT ACCCCATGGA 8951 CTCACAACTG CTCCAACAGC AGCTGTGTGA ACACCCCGGG CTCGTTTAAG 9001 TGCTCCTGTC AGGATGGTTT TCGTCTGACG CCTGAGCTGA GCTGCACTGA 9051 TGTGGATGAG TGCTCAGAGC AGGGGCTCAG TAACTGTCAT GCCCTGGCCA 9101 CCTGTGTCAA CACAGAAGGC GACTACTTGT GCGTGTGTCC CGAGGGCTTT ACAGGGGATG GTTGGTACTG TGAGTGCTCC CCAGGCTCCT GTGAGCCAGG 9151

			POI	LYCLONING SI	TE OF pbs
9301	GGTGTGGGCT	ACTCCTGTGA			
9251	CCTGCAATAC	ATATGAGACC	CTGACTGAGT	ACTGGCGCAG	CACAGAGTAT
9201	ACTGGACTGC	TTGCCCCAGG	GCCCGGATGG	AAAGCTGGTG	TGTCAAGACC

FIG.10H

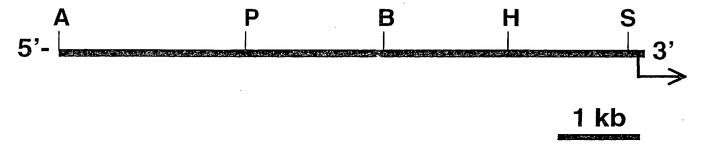


FIG. 11

1 TACTGGCGCA GCACAGAGTA CGGCTCCGGC TACGTCTGTG ATGTCAGTCT
ASIA
51 GGGCGGCTGG TACCGCTTCG TGGGCCAGGG CGGCGTGCGC CTGCCCGAGA
101 CCTGCGTGCC CGTCCTGCAC TGCAACACGG CCGCGCCTAT GTGGCTCAAC
151 GGCACGCACC CATCGAGCGA CGAGGGCATC GTGAACCGCG TGGCCTGTGC
201 GCACTGGAGC GGCGACTGCT GCCTGTGGGA CGCGCCTGTC CAAGTGAAGG
251 CCTGTGCCGG CGGCTACTAC GTGTACAACC TGACAGAGCC CCCTGAG
.ASI7

FIG.12

1	ACTATAGGGC	ACGCGTGGTC	GACGGCCCGG	GCTGGTAAAT	<u>CTT</u> AAAAAAA
		_	AS		
51	AAAAAAAACA	AAAAGAACAT		CCCTGCCCTG	GCACTTTATT
				A52	
101	GGAAGGTCAA	GAACACACTC	AACCACACAA	GAGATGTGAA	CATACCTGTG
		AS3			~
151	TGGTACCCAA	AGACATCCCC	TTTCACACAT	ACATGACCCT	TCCATTGGGT
		AS4			115
201	TGCACATTGC	TGTTAGCTTT	TTGTTGGAGA	AGGGAGCTAG	AS 5 ACACCTCTAC
251	ACAACCCCCA	ACTGGAGTTC	TCTGGAACAG	AGTAAATACC	ATCGTGTCAT
301	CATGGAGCGC	ACACACACTG	TGGTCCTGCA	ACCTCGATTT	GTGTCCTGGC
351	TCTGCTGCTT	ACCAATGAAG	CAAGTAGCTT	AAACCTTCTG	AATCTCAAGT
101	TTCCTCACCC	TCAAACTATA	GCTAAATACA	AAAGTCATTT	CCCAGGGCCA
51	COCCACACCA	<b>Ш</b> ШФШ 2 ШФ 2 Ф 2	m,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		
FOT	ADDADADDTO	TTCTATCAGA	TAATGGATAG	AAGATGCCTA	TCCCAGTGTT
01	TGACATATCC	TAAGTGCTTA	ATACACGAGA	GCTCACCATC	<b>ΤΤΤΑ CTCCTA</b>
				001011001110	TITICICOIA
C 1	mm2.mmc.c2.c2	G1G111G1G1			
51	TTATTGCACA	GAGAAACACA	CAAAGTGTCA	GTGCCCCTGC	TAGGTAGAGA
01	GGGANGCANG	GNAAGGAGAT	CTGAGCAAAA	GGCATAGAAT	ΑΨΑΨΟΑΑΘΟΨ
					11111 CAAGC I
51	GGG		_		

FIG.13A

```
1 CGGGGGAAGG TTTATTTTGT TTCTTTCAA AGGGGGTCTT GNTCTGTCTC
51 AAAGACCNTA AGGACCATGA AAAAATCTCT TTGTNAAAAG TGCCAAGCGG
101 TCCCCACTCT GAATCTGGGC TTTTCTGCCT GCAGAAAGCT GCTCTGAATG
151 TCACGCCAAT GCCACTTGTA CGGTGGACGG GGCTTGCCAC GACCTGCGCC
201 TGCCAGGAGG GCTTCACTGC GACGGCCTCG AATGTGCGGA TCTGGATGAA
251 TGCGCATTC TGGGGGCGCA CAACTGCTCC GCCACCAACA GCTGCGTGAA
301 CGCGCTGGGC TCCTACACAT GCGTCTGCCC TGAAGGTTTC CTCCTGAGCT
351 CGGAGCTCGG CTGCGAGGAT GTGCAGAGGC AGGGCTCAGC
401 CGCTGCCAC CCCTGGCCAC CTGCATCAAT GGCGAGGGCA ACTACTCATG
451 CGTGTGTCCC GCGGGCTACG TGGGGGACGG GAGGCACTGT GAGTGTTCCC
501 CGGGCTCCTG CGGGCCTACG TGGGGGACGG TGACGCGCTA
551 GTGTGCGCTG ACCCGTGCCA GGCGCACCAC ATCCTGGACG AATACTGGCG
601 CAGCACAGAG TACGGCTCCG GCTACGTCTG TGATGTCAGT CTGGGCGGCT
```

FIG. 13B

ACTATAGGGC ACGCGTGGTC GACGGCCCGG GCTGGTAAAG ACACCCAGAC 1 TTAGGTTTTG ACAGAGCCTC ATGTTCACCA ACCAGAAATG ACATTCACCA 51 CCTAGGATTG AGAAAAAGAA TATTAGGAAC TTTTATTTTC TTCTGAAGTT 101 151 ATAGCAAAGA AAGGGGAAAA AAAAAAACAT TCTTATGGGG GATAAACGGG CAAAGGATAC AAACAGTTCA GAAAAGAATA AATAGTAAGC AAATGAAAAG 201 ATAACTTCCT TTTTCATCAA AGAACCGCAA AAGTAAATAA TGATAAGATG 251 TTTCTCACTT TTCCACAAAG ATGAAAGTTA ATGCCCAGGG TGGCTGAGTA 301 351 CTGTGCTGGG ATTGTGAACT AACTGTTATA GATCTCTCTG GGGTGCTGTT TGGGAAGAAA CATCGCTGAA AACTGAGCTA CCTCTTTTCC TATGAAATTC 401 CCCTGAGGAG GTGAGTGAGC CGCTGCTGAT CGTCACCCGA GCACTAGGCC 451 AGACAGÁAGG AGAAAGCCCT CAAAGAGGCA ATGCTGTGGA TCACTGTCAT 501 ATTTCCTGCT CAGCCTGAGT TCACATGTGC CTGATTTTTC TCAATATGGC 551 ATTGCCATTA ACGTGGAATT AGGTCAGGAG ACCTAAGGCT GAACCAAGCC 601 CTGTCATTCT CTGCCCCATG ACTGCGCATC ACCAAAACAG CATCGGCAGT 651 GACTTCCACA GATGGTACCA TTGCTATATG CCTTAACTTG CATCATCTCC 701 TTTAATGGCC ATAACAATTC TAGGACACGG GTATTCTTGT TTTACAGATG 751 ATGAAAATTA CCTCTGGAAG GAAAATTACT GGCACACAAA AAACGCTGAC 801 CAGGATTCAG ATAGACTGAC TCCAAAGTCA GTCTGTTCAT CTACAAAATT 851 901 ATCTACTTCT CAAGGACCTT CCTTCATGGG AATTCAAATT TCTTGATTCA 951 CAGAGCATCT GGTCCAATGA TGTCTGAATT ATCTGCTGTC TCTGACCTTC

FIG. 14A

AGCCATTCTC AGCTCCTTC CTGATCACAT TGGGACCCCA GGGGAGCTGG

1051 CTGAATCTGT GAGGATGGCA TTTGCTTTGG AATTAAGTGG CCACAAGTAC

1101 ACATCCTGGT GGGGACGATG AGCACCCCTT TTCTCCTGGA GCAGCCTGGC

1151 TTCAGATTCT GGCCTCTGCT TGGCTCCACT TTGTGCTTTT CAATGACCAA

1201 GAAAATCCCA GGCCCTTGGA ATTGTTTACT CAGTTAATTT CTAACTAAAG

1251 AACCTCTTGT TGCCAAAAGG TATAAAACAG AGCCCTTGTA GCTGTGGGCA

1301 CAGCTGTGAC CCCCATGTCA ATCATTTGGG GTCTCTACCT ATTAGGGAAA

1351 AGAACAACAA CCACCTCACA GCCTAGAAAA GGAAAACACT GTGTCAAAAG

1401 GGAAAAATAT TCCACCCCCA TTAAAAATAAT TAAGAAAACAG AACCAGAGGA

1451 TCATTGGAGG AGAGATTGCC AGTGGGGGAC AGATGTATAT ATATAGATAT

1501 GAAAGTCACC TACTTGTAAA AGGATTAATT CTACCTTTCT GGTTTCAGGT

1551 AAGGCTATCT GCAGCTCTCA CTTCTCCTAG CCACTTCTCC CATCTAGTCT

FIG. 14B

```
$ type guromodulinpromoter18full.pair;1
 BESTFIT of: Guromodulinpromoter18full check: 3852 from: 1 to: 1630
 to: mouseThppromoterfull. check: 5595 from: 1 to: 9343
 Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Swgapdna.Cmp
 CompCheck: 2335
                                                        Average Match: 10.000
                                          50
               Gap Weight:
                                                   Average Mismatch: -9.000
          Length Weight:
                                                                    Length:
                                     1617
                    Ouality:
                                                                                         15
                        Ratio: 3.177
                                                                        Gaps:
  Percent Similarity: 74.385 Percent Identity: 74.385
              Match display thresholds for the alignment(s):
                                   = IDENTITY
                                             7
  Guromodulinpromoter18full x Thppromoterfull. March 24, 2000 16:31 ...
       6677 AACATTCCTTTTTTCCTAACACAGTCTGACTTCAGATATACTGTCTTTTT 6726
       1158 TCTGGCCTCT...GCTTGGCTCCACTTTGTGCTTTTCAATGACCAAGAAA 1204
                  6727 CCTGGCTCCTTGGGCTTAGGTCTACCTTGTCCTTGCCCAGGTCCAAGAAA 6776
       6777 AGGCCCAGAACCTTGGCACTGTTTTGCCAGTTAATGTCTAACTGAGGAAT 6826
       1254 CTCTTGTTGCCAAAAGGTATAAAACAGAGCCCTTGTAGCTGTGGGCACAG 1303
                  6827 GTCTTGCTGCCAAAAGGT.GAAAACAGAGACCTTGTATTTCCAGGCACAG 6875
        1304 CTGTGACCCCCATGTCAATCATTTGGGGTCTCTACCTATTAGGG...AAA 1350
                   6876 GTGTGACCCCAATGTCAATCATTT . TGTGTCTAACTCCCAGGGGAAAAA 6923
        1351 AGAACAACCACCTCACAGCCTAGAAAAGGAAAACACTGTGTCAAAAG 1400
                    6924 CTAACAACAGACTCATGGCTTGGAAAAGGTGAATTCTATGCCAAAAG 6973
        1401 GGAA.AAATATTCCACCCCATTAAAATAAT.TAAGA.AACAGAACCAGA 1447
        1498 TATGAAAGTCACCTACTTGTAAAAGGATTAATTCTACCTTTCTGGTTTCA 1547
                   11 | 1 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 
         7071 GATCACAGGCACTTACTTGTGAATGGACCAGTCCT...GTCCTGGGTTCA 7117
```

1548	GGTAAGGCTATCTGCAGCTCTCACTTCTCCTAGCCACTTCTCCCATCT	1595
1340		
7110	GGTAAGGCTGTATGAAACTGTCAC.CCCCATATCCACTTCTCCTCTATCT	7166
/110	GGIAAGGCIGIAIGAAACIGICAC.CCCC	
1596	AGTCTTTGCTGGCTCCCATTCTGTTTGAAGGATG 1629	
7167	AATCCCATTATATTTCAGGGAGG 7189	
1 - 0 1	C	

FIG.15B

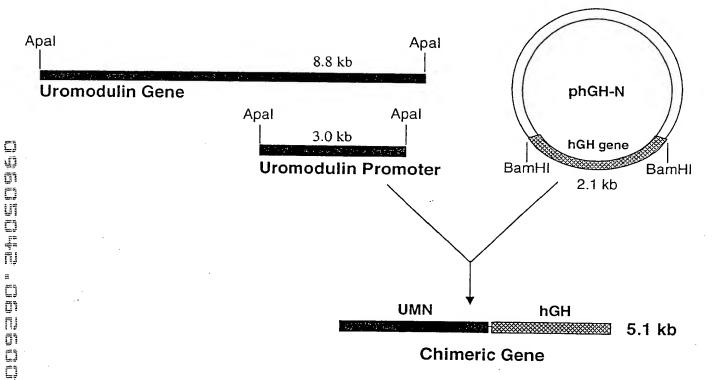


FIG. 16

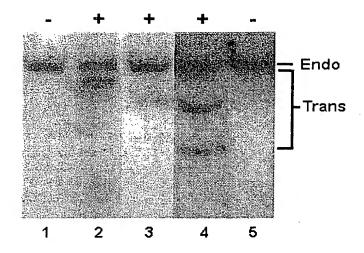


FIG.17

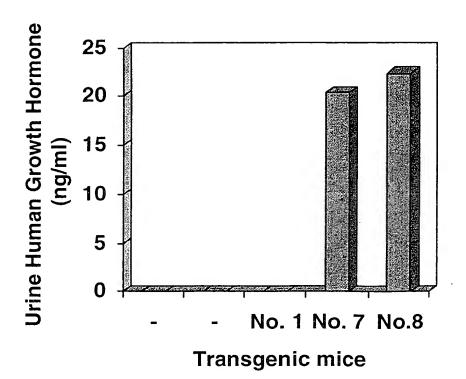


FIG.18

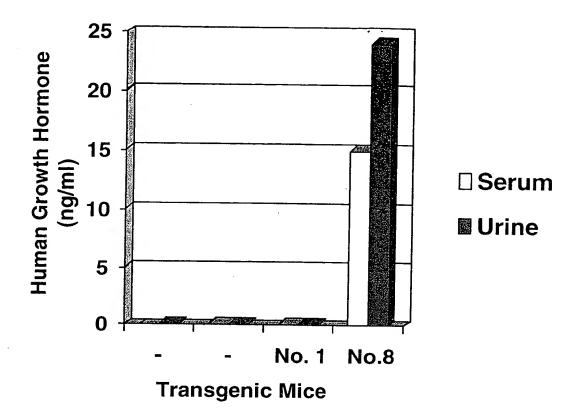


FIG.19

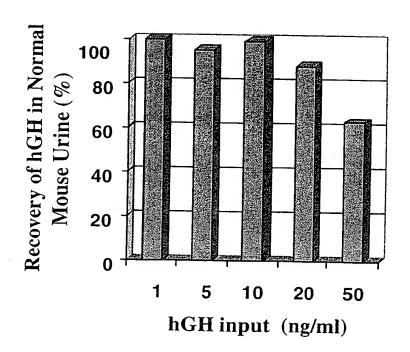


FIG.20